Osteoporosis Risk Prediction

The aim of this project is to predict the risk of osteoporosis in patients using a dataset of patients' medical records. Osteoporosis is a condition that weakens bones, making them fragile and more likely to break. It develops slowly over several years and is often only diagnosed when a minor fall or sudden impact causes a bone fracture. The condition is more common in older people, particularly.

About the dataset

The dataset offers comprehensive information on health factors influencing osteoporosis development, including demographic details, lifestyle choices, medical history, and bone health indicators. It aims to facilitate research in osteoporosis prediction, enabling machine learning models to identify individuals at risk. Analyzing factors like age, gender, hormonal changes, and lifestyle habits can help improve osteoporosis management and prevention strategies.

Data Dictionary

Column	Description
ID	Unique identifier for each patient
Age	Age of the patient
Gender	Gender of the patient
Hormonal Changes	Whether the patient has undergone hormonal changes
Family History with Osteoporosis	Whether the patient has a family history of osteoporosis
Race/Ethnicity	Race or ethnicity of the patient
Body Weight	Weight details of the patient
Calcium	Calcium levels in the patient's body
Vitamin D	Vitamin D levels in the patient's body
Physical Activity	Physical activity details of the patient
Smoking	Whether the patient smokes
Alcohol Consumption	Whether the patient consumes alcohol
Medical Conditions	Medical conditions of the patient
Medication	Medication details of the patient
Prior Fracture	Whether the patient has had a prior fracture
Osteoporosis	Whether the patient has osteoporosis

Potential analysis in this project

- **Predictive Modeling**: Develop machine learning models to predict the probability of osteoporosis based on the provided features. This analysis is crucial for identifying individuals at risk of osteoporosis, enabling early intervention and prevention strategies.
- **Feature Importance Analysis**: Determine the importance of each feature in predicting osteoporosis risk. Understanding which factors have the most significant impact on osteoporosis risk can provide insights into the underlying mechanisms and guide targeted interventions.
- **Correlation Analysis**: Examine correlations between different features and osteoporosis risk. Identifying strong correlations can help identify potential risk factors or associations that may warrant further investigation or intervention.
- **Subgroup Analysis**: Analyze how osteoporosis risk varies across different subgroups based on demographics, lifestyle factors, or medical history. Understanding how risk factors interact within different population groups can inform personalized approaches to osteoporosis prevention and management.
- **Model Interpretation**: Interpret the trained models to understand how different features contribute to osteoporosis risk prediction. This analysis can provide insights into the underlying relationships between variables and help healthcare professionals make informed decisions regarding patient care and management strategies.

In [ ]:
```
#importing the required libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

In [ ]:
```
#Loading the dataset
df = pd.read_csv("osteoporosis.csv")
df.head()
```

Out[ ]:

	Id	Age	Gender	Hormonal Changes	Family History	Race/Ethnicity	Body Weight	Calciu Intak
0	104866	69	Female	Normal	Yes	Asian	Underweight	Lo
1	101999	32	Female	Normal	Yes	Asian	Underweight	Lo
2	106567	89	Female	Postmenopausal	No	Caucasian	Normal	Adequat
3	102316	78	Female	Normal	No	Caucasian	Underweight	Adequat
4	101944	38	Male	Postmenopausal	Yes	African American	Normal	Lo

Data Preprocessing Part 1

In [ ]:
```
#checking the shape of the dataset
df.shape
```

Out[ ]: (1958, 16)

In [ ]:
```
#checking the information of the dataset
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1958 entries, 0 to 1957
Data columns (total 16 columns):
 #   Column               Non-Null Count  Dtype 
---  ------               --------------  ----- 
 0   Id                   1958 non-null   int64 
 1   Age                  1958 non-null   int64 
 2   Gender               1958 non-null   object
 3   Hormonal Changes     1958 non-null   object
 4   Family History       1958 non-null   object
 5   Race/Ethnicity       1958 non-null   object
 6   Body Weight          1958 non-null   object
 7   Calcium Intake       1958 non-null   object
 8   Vitamin D Intake     1958 non-null   object
 9   Physical Activity    1958 non-null   object
 10  Smoking              1958 non-null   object
 11  Alcohol Consumption  970 non-null    object
 12  Medical Conditions   1311 non-null   object
 13  Medications          973 non-null    object
 14  Prior Fractures      1958 non-null   object
 15  Osteoporosis         1958 non-null   int64 
dtypes: int64(3), object(13)
memory usage: 244.9+ KB
```

Few columns have missing values, so before proceeding with the analysis, I will first handle the missing values in the dataset.

In [ ]:
```
#columns with missing values
columns_with_missing_values = df.columns[df.isnull().any()]

#missing value percentage
print("Missing value percentage")
for column in columns_with_missing_values:
    print(column,":",df[column].isnull().sum()/df.shape[0]*100)
```

```
Missing value percentage
Alcohol Consumption : 50.45965270684371
Medical Conditions : 33.04392236976506
Medications : 50.30643513789581
```

Alcohol Consumption and Medications columns have more than 50% missing values, I will be replacing these missing values with "None" as it is possible that the patient does not consume alcohol or take any medications. The same goes for the Medical Conditions column.

However, the columns with more than 50% missing values might not be much useful for the analysis, but still I am keeping them for the remaining 50% of the data.

In [ ]:
```
#replace missing values with "None"
df.fillna("None",inplace=True)
```

The column ID is an identifier and irrelevant for the analysis, so I will drop this column.

In [ ]:
```
df = df.drop(['Id'], axis=1)
```

In [ ]:
```
#value counts of categorical columns
categorical_columns = df.select_dtypes(include=['object']).columns
for column in categorical_columns:
    print(df[column].value_counts())
```

```
Gender
Male      992
Female    966
Name: count, dtype: int64
Hormonal Changes
Normal            981
Postmenopausal    977
Name: count, dtype: int64
Family History
No     998
Yes    960
Name: count, dtype: int64
Race/Ethnicity
African American    681
Caucasian           646
Asian               631
Name: count, dtype: int64
Body Weight
Normal         1027
Underweight     931
Name: count, dtype: int64
Calcium Intake
Low         1004
Adequate     954
Name: count, dtype: int64
Vitamin D Intake
Sufficient      1011
Insufficient     947
Name: count, dtype: int64
Physical Activity
Active       1021
Sedentary     937
Name: count, dtype: int64
Smoking
Yes    982
No     976
Name: count, dtype: int64
Alcohol Consumption
None        988
Moderate    970
Name: count, dtype: int64
Medical Conditions
Hyperthyroidism         678
None                    647
Rheumatoid Arthritis    633
Name: count, dtype: int64
Medications
None               985
Corticosteroids    973
Name: count, dtype: int64
Prior Fractures
Yes    983
No     975
Name: count, dtype: int64
```

Descriptive Statistics

In [ ]:
```
df.describe()
```

Out[ ]:

	Age	Osteoporosis
count	1958.000000	1958.000000
mean	39.101124	0.500000
std	21.355424	0.500128
min	18.000000	0.000000
25%	21.000000	0.000000
50%	32.000000	0.500000
75%	53.000000	1.000000
max	90.000000	1.000000

In [ ]:
```
df.head()
```

Out[ ]:

	Age	Gender	Hormonal Changes	Family History	Race/Ethnicity	Body Weight	Calcium Intake	Vitan Ir
0	69	Female	Normal	Yes	Asian	Underweight	Low	Suff
1	32	Female	Normal	Yes	Asian	Underweight	Low	Suff
2	89	Female	Postmenopausal	No	Caucasian	Normal	Adequate	Suff
3	78	Female	Normal	No	Caucasian	Underweight	Adequate	Insuff
4	38	Male	Postmenopausal	Yes	African American	Normal	Low	Suff

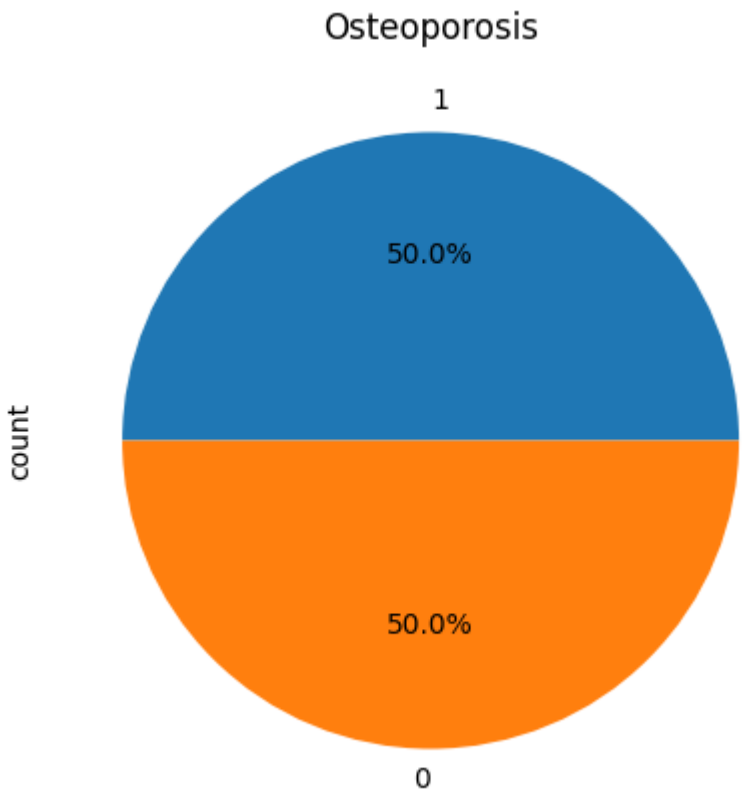
Exploratory Data Analysis

In the exploratory data analysis, I will be looking at the distribution of the data acroos all the variables and relationships between the variables and the target variable. For this I will be plotting the dataset variables in different graphs and draw out insights from them

Target Variable Distribution

In [ ]:
```
#pie chart for the target variable (Osteoporosis)
plt.figure(figsize=(5,5))
df['Osteoporosis'].value_counts().plot.pie(autopct='%1.1f%%').set_title('Osteopo
```

Out[ ]:
```
Text(0.5, 1.0, 'Osteoporosis')
```

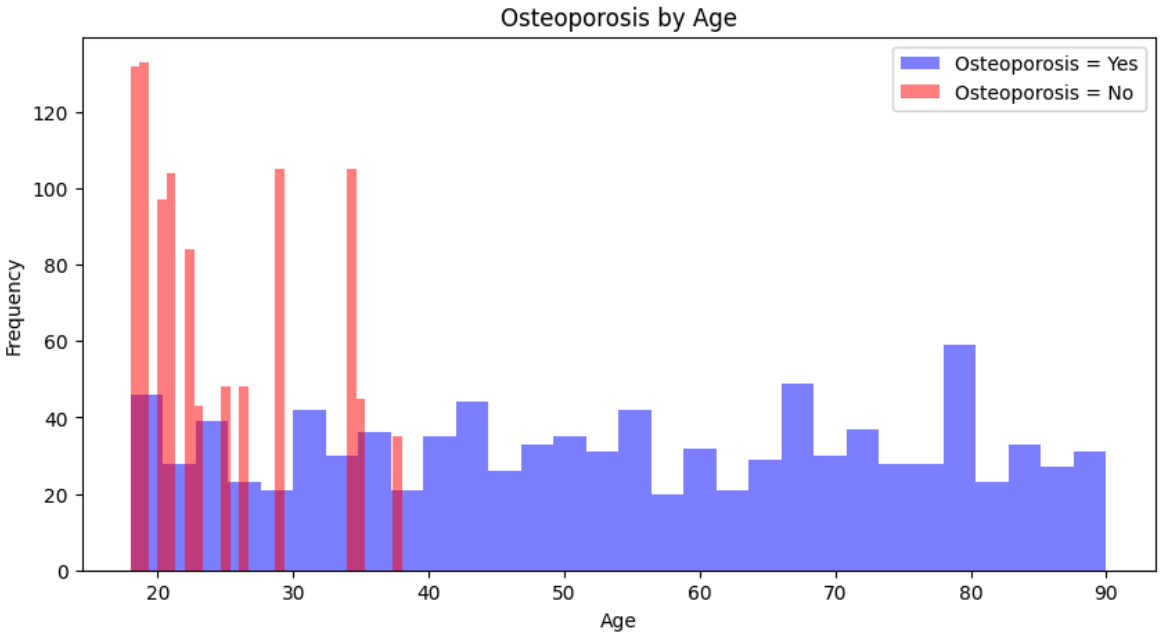


The above pie chart shows that the dataset is perfectly balanced with 50% of the patients having osteoporosis and 50% not having osteoporosis, which means that the dataset is not biased towards any class.

Age and Osteoporosis

In [ ]:
```
#two layer histogram for the Age and Osteoporosis
plt.figure(figsize=(10,5))
df[df['Osteoporosis']==1]['Age'].plot.hist(bins=30, alpha=0.5, color='blue', lab
df[df['Osteoporosis']==0]['Age'].plot.hist(bins=30, alpha=0.5, color='red', labe

#legends and title
plt.legend()
plt.xlabel('Age')
plt.title('Osteoporosis by Age')
```

Out[ ]:
```
Text(0.5, 1.0, 'Osteoporosis by Age')
```

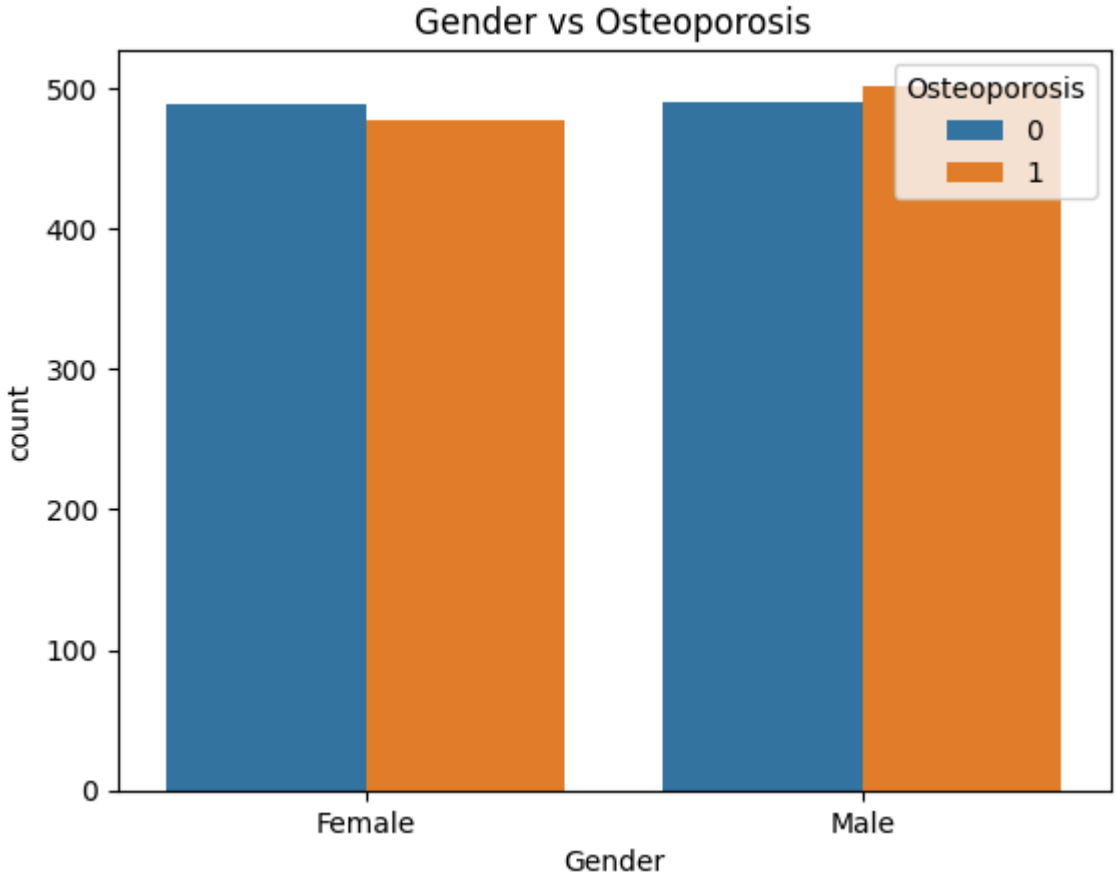


This graph shows relation between the risk of osteoporosis and the age of the patient. In the graph we can see that that there is significant risk of osteoporosis in patients of all ages but patients between the ages 20 to 40 have significantly much lower risk of osteoporosis. This highlights that fact that younger patients are less likely to have osteoporosis.

Gender and Osteoporosis

In [ ]:
```
sns.countplot(x='Gender', data=df, hue='Osteoporosis').set_title('Gender vs Oste
```

Out[ ]:
```
Text(0.5, 1.0, 'Gender vs Osteoporosis')
```

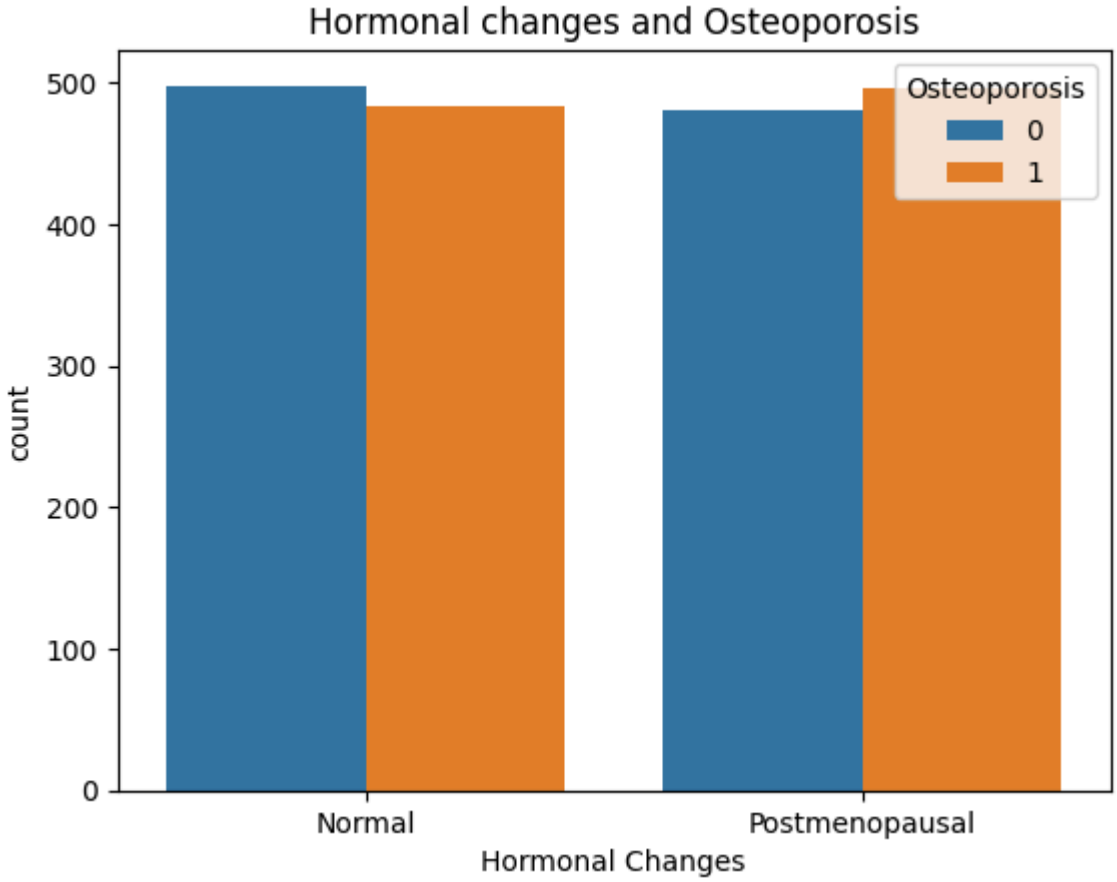


In this graph, we can visualize the relationship between gender and the risk of osteoporosis. The graph shows that there is no concrete relationship between gender and the risk of osteoporosis, however, according to the numbers in the dataset, the males tend to have slightly higher number of osteoporosis cases than females, but the difference is not significant. Therefore, gender could be a weak predictor for osteoporosis.

Hormonal Changes and Osteoporosis

In [ ]:
```
#hormonal changes and Osteoporosis
sns.countplot(x='Hormonal Changes',data=df,hue='Osteoporosis').set_title('Hormon
```

Out[ ]:
```
Text(0.5, 1.0, 'Hormonal changes and Osteoporosis')
```



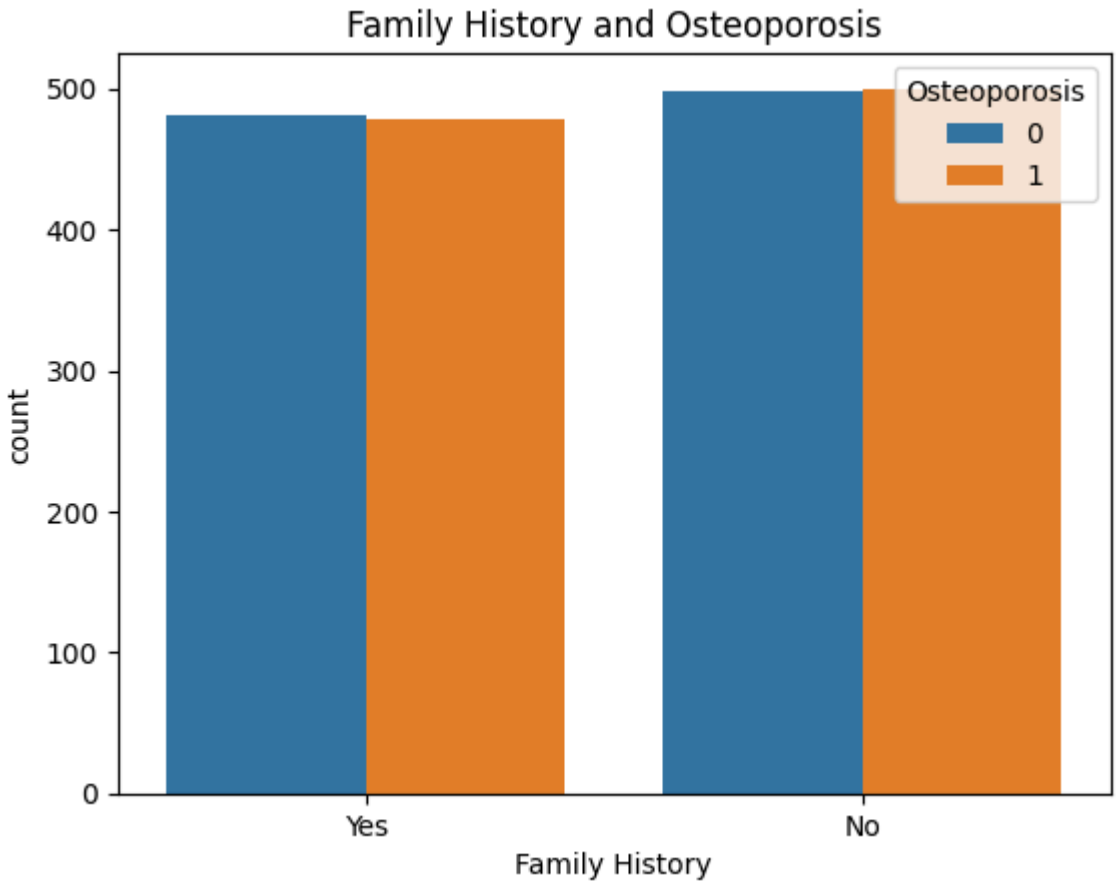
Note: Here Postmenopausal is not only for females, but it also reflects the cap on testosterone production in males, therefore for both genders, the hormonal changes are termed as postmenopausal.

The graph shows that patients who have undergone hormonal changes have a higher risk of osteoporosis than those who have not undergone hormonal changes. This indicates that hormonal changes can be a significant risk factor for osteoporosis. This highlights that our hormones contribute in making our bones strong

Family History and Osteoporosis

In [ ]:
```
sns.countplot(x = "Family History", data = df, hue = "Osteoporosis").set_title("
```

Out[ ]:
```
Text(0.5, 1.0, 'Family History and Osteoporosis')
```

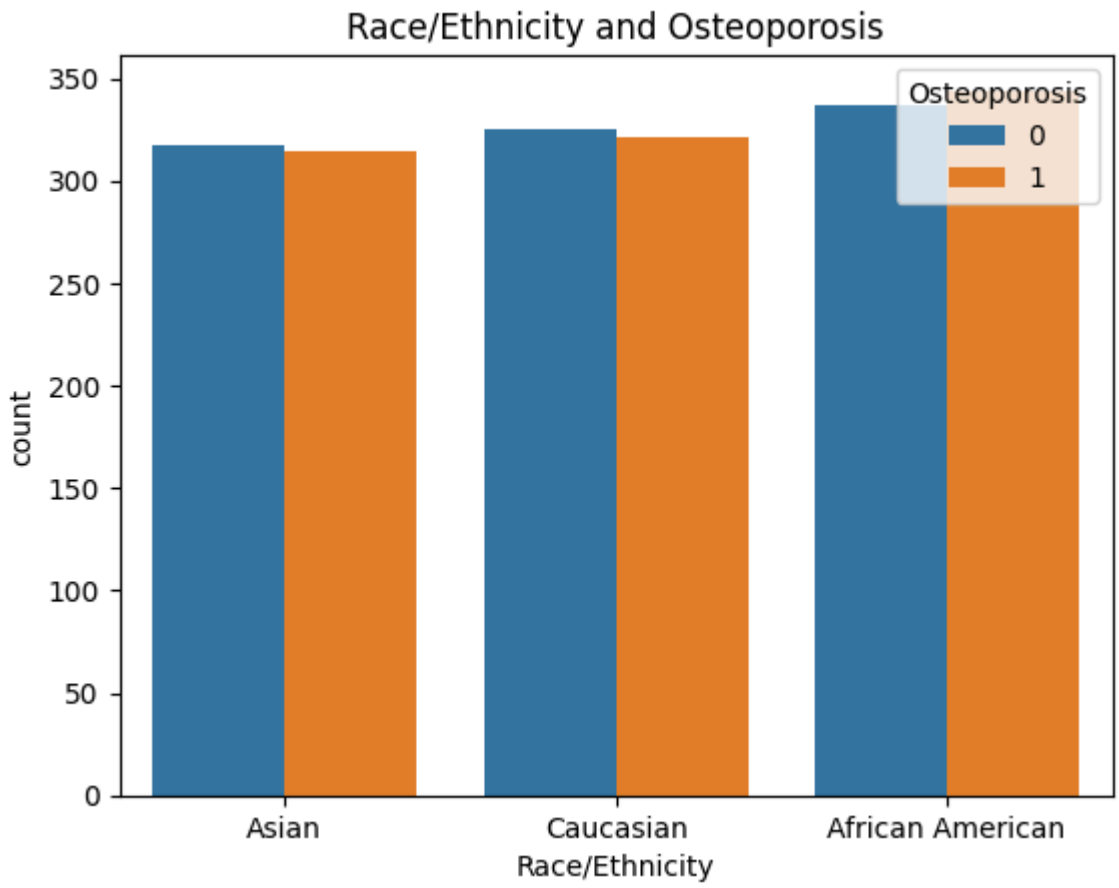


It is believed that genetics play a important role in the development of a disease. The graph shows the relationship between family history of osteoporosis and the risk of osteoporosis. But in the graph there is not much differnece in both cases regarding the risk of osteoporosis. Therefore, family history couldn;t be considered a predictor for osteoporosis.

Race/Ethnicity and Osteoporosis

In [ ]:
```
sns.countplot(x="Race/Ethnicity", data = df, hue = "Osteoporosis").set_title("Ra
```

Out[ ]:
```
Text(0.5, 1.0, 'Race/Ethnicity and Osteoporosis')
```

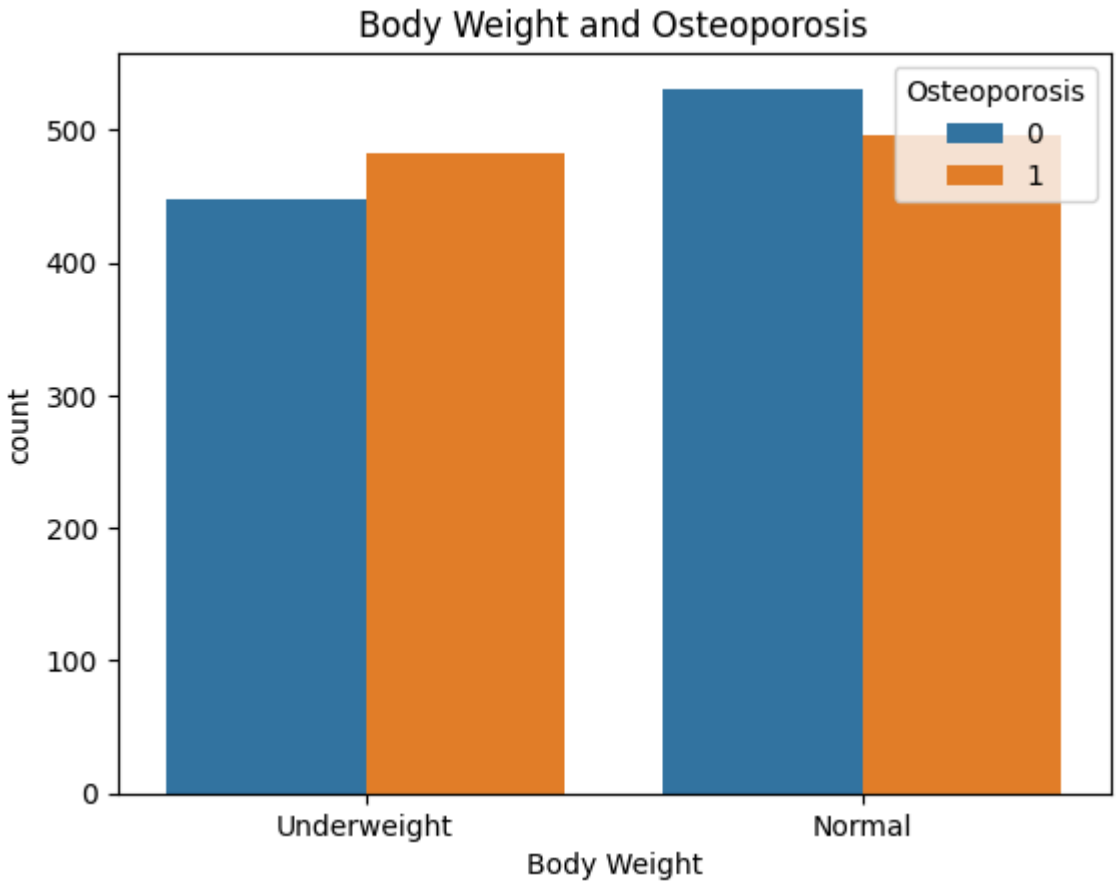


This graph shows the relationship between Race/Ethnicity and the risk of osteoporosis. The graph shows that the risk of osteoporosis is almost similar with no concrete relationship between the race and risk of osteoporosis.

Body Weight and Osteoporosis

In [ ]:
```
sns.countplot(x="Body Weight", data = df, hue = "Osteoporosis").set_title("Body
```

Out[ ]:
```
Text(0.5, 1.0, 'Body Weight and Osteoporosis')
```

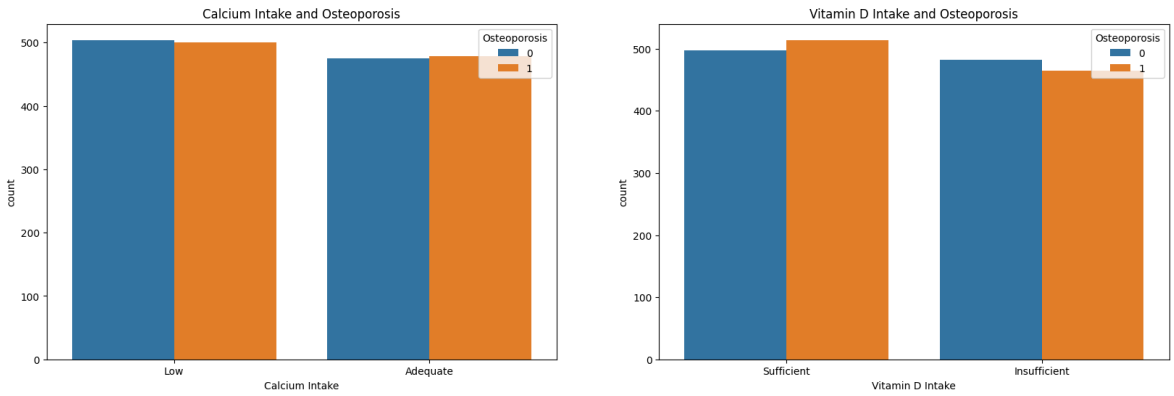


Body weight is an important factor in determining the risk of osteoporosis. The graph shows that patients with lower body weight have a higher risk of osteoporosis than those with higher body weight. This indicates that body weight can be a significant risk factor for osteoporosis. This highlights that our body weight contributes in making our bones strong.

Nutrition and Osteoporosis

In [ ]:
```
fig, ax = plt.subplots(1, 2, figsize=(20, 6))
sns.countplot(x='Calcium Intake', data=df, ax=ax[0], hue='Osteoporosis').set_tit
sns.countplot(x='Vitamin D Intake', data=df, ax=ax[1], hue='Osteoporosis').set_t
```

Out[ ]:
```
Text(0.5, 1.0, 'Vitamin D Intake and Osteoporosis')
```



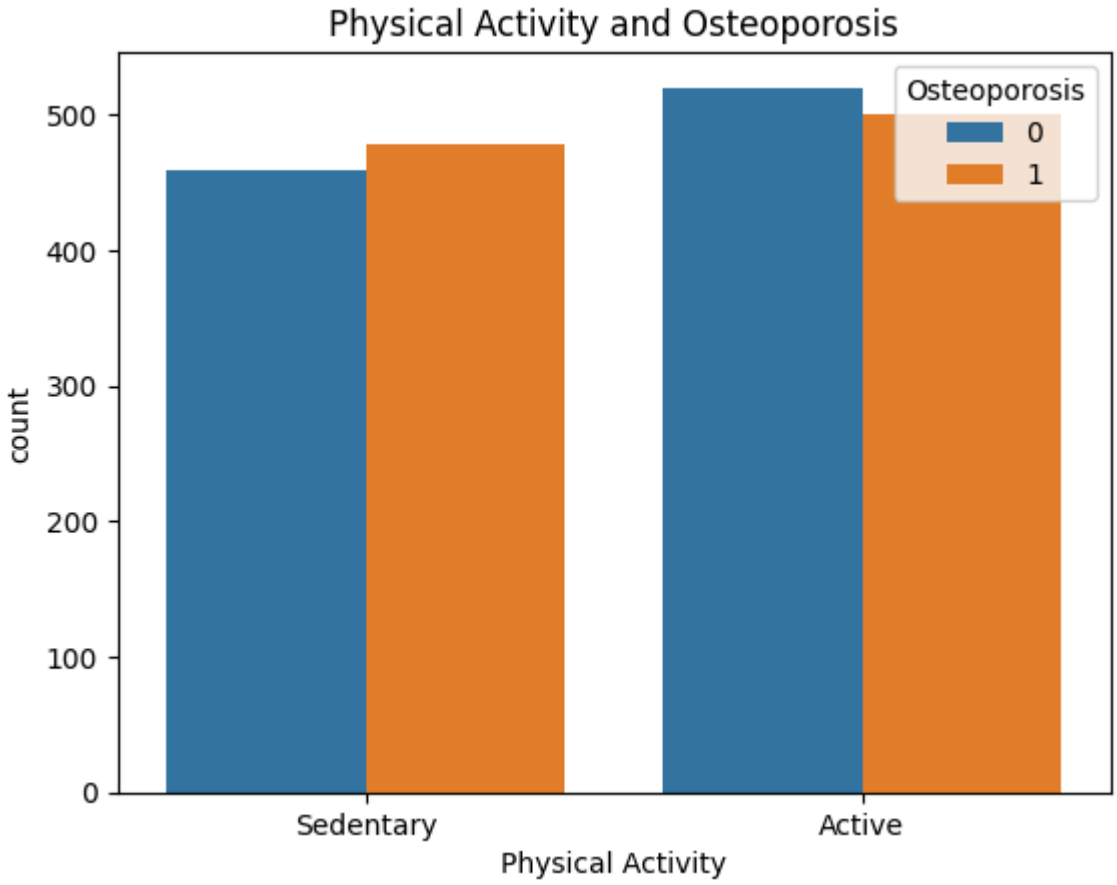
Nutrition and Osteoporosis are closely related. The graph shows that patients with lower calcium and vitamin D levels have a higher risk of osteoporosis than those with higher calcium and vitamin D levels. This indicates that nutrition can be a significant risk factor

for osteoporosis. This highlights that our nutrition contributes in making our bones strong.

Physical Activity and Osteoporosis

In [ ]:
```
sns.countplot(x='Physical Activity', data=df, hue='Osteoporosis').set_title('Phy
```

Out[ ]:
```
Text(0.5, 1.0, 'Physical Activity and Osteoporosis')
```

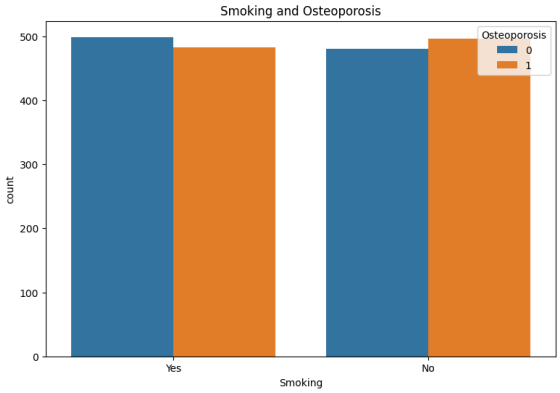


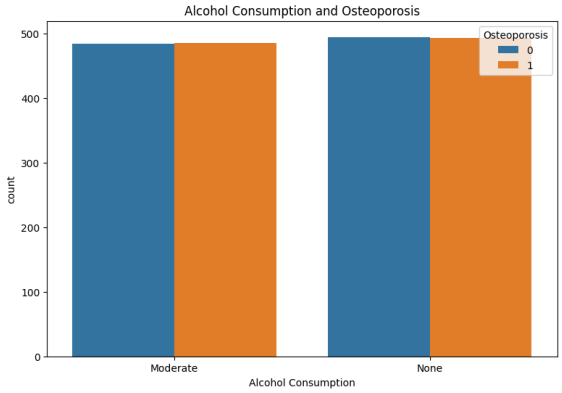
Physical Activity and Osteoporosis have a relation between them. The graph shows that patients with active physical acitve lifestyle lower risk of osteoporosis as compared to the patients with sedentary lifestyle.

Smoking and Alcohol Consumption and Osteoporosis

In [ ]:
```
fig, ax = plt.subplots(1, 2, figsize=(20, 6))
sns.countplot(x='Smoking', data=df, ax=ax[0], hue='Osteoporosis').set_title('Smo
sns.countplot(x='Alcohol Consumption', data=df, ax=ax[1], hue='Osteoporosis').se
```

Out[ ]:
```
Text(0.5, 1.0, 'Alcohol Consumption and Osteoporosis')
```



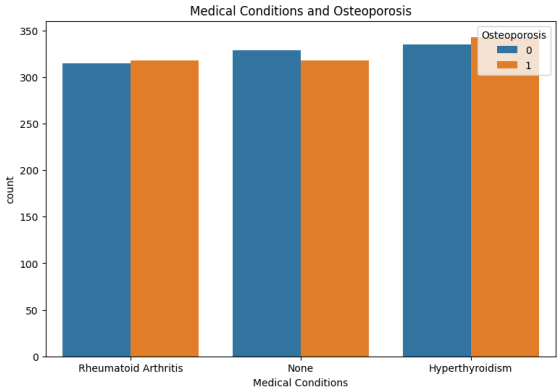


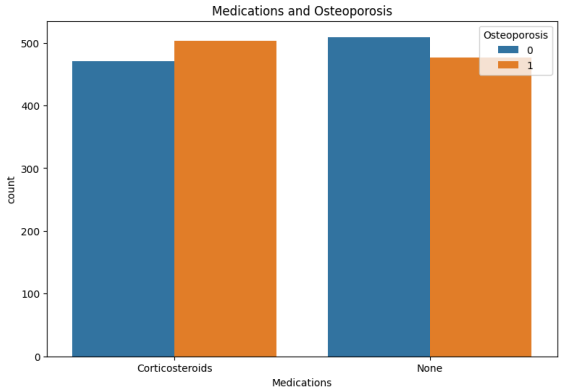
Smoking and Alcohol Consumption are one of those factors that could have adverse effect on a patients health. Here, the graph shows that patients who smoke and consume alcohol does not relate to the risk of osteoporosis. This indicates that smoking and alcohol consumption are not significant risk factors for osteoporosis.

Medical Conditions and Medications and Osteoporosis

In [ ]:
```
fig, ax = plt.subplots(1, 2, figsize=(20, 6))
sns.countplot(x='Medical Conditions', data=df, ax=ax[0], hue='Osteoporosis').set
sns.countplot(x='Medications', data=df, ax=ax[1], hue='Osteoporosis').set_title(
```

Out[ ]:
```
Text(0.5, 1.0, 'Medications and Osteoporosis')
```



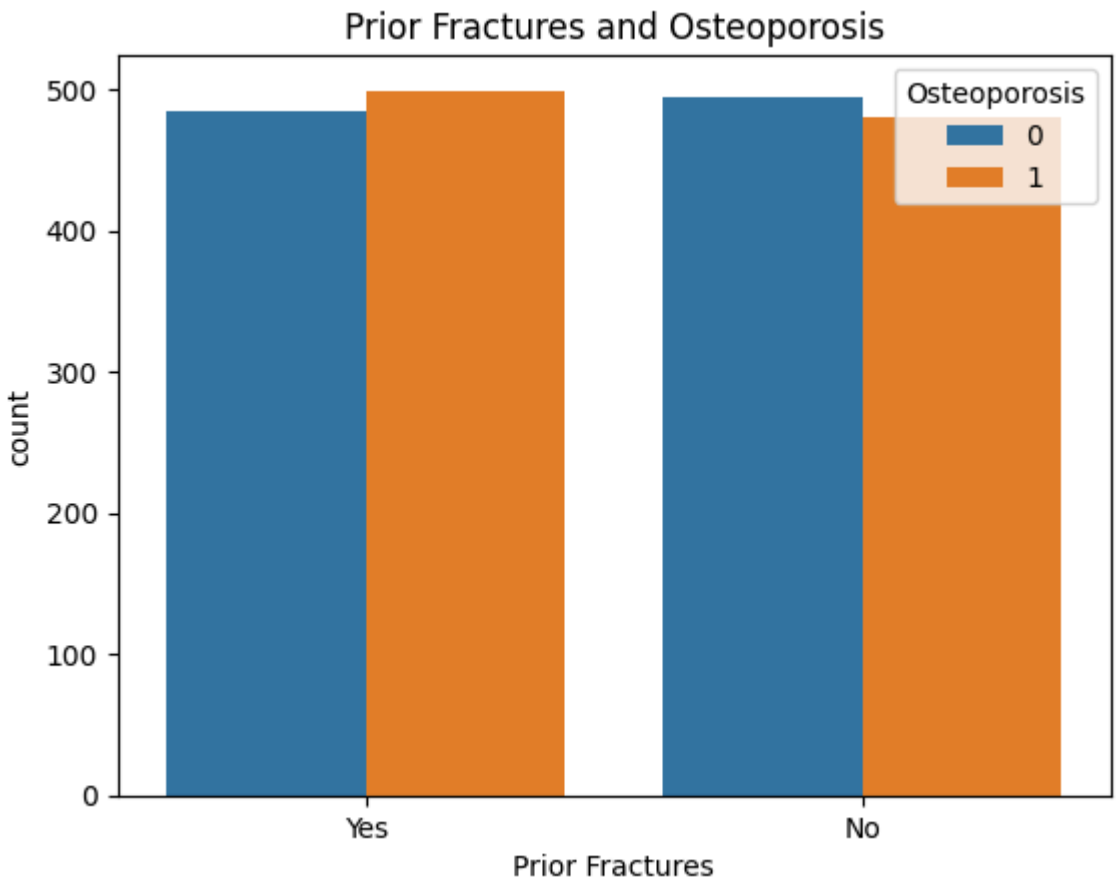


The graph shows that patients with medical conditions like Hyperthyroidism have a higher risk of osteoporosis than those without medical conditions. This indicates that medical conditions can be a significant risk factor for osteoporosis. In addition to that patients who consume medications like Corticosteriods have higher risk of osteoporosis.

Prior Fracture and Osteoporosis

In [ ]:
```
sns.countplot(x='Prior Fractures', data=df, hue='Osteoporosis').set_title('Prior
```

Out[ ]:
```
Text(0.5, 1.0, 'Prior Fractures and Osteoporosis')
```



This graph shows the relation between the prior incident of fractures and risk of osteoporosis and from the graph it is clear that there is no concrete relationship between the prior incident of fractures and risk of osteoporosis.

Data Preprocessing Part 2

Label Encoding the Categorical Variables

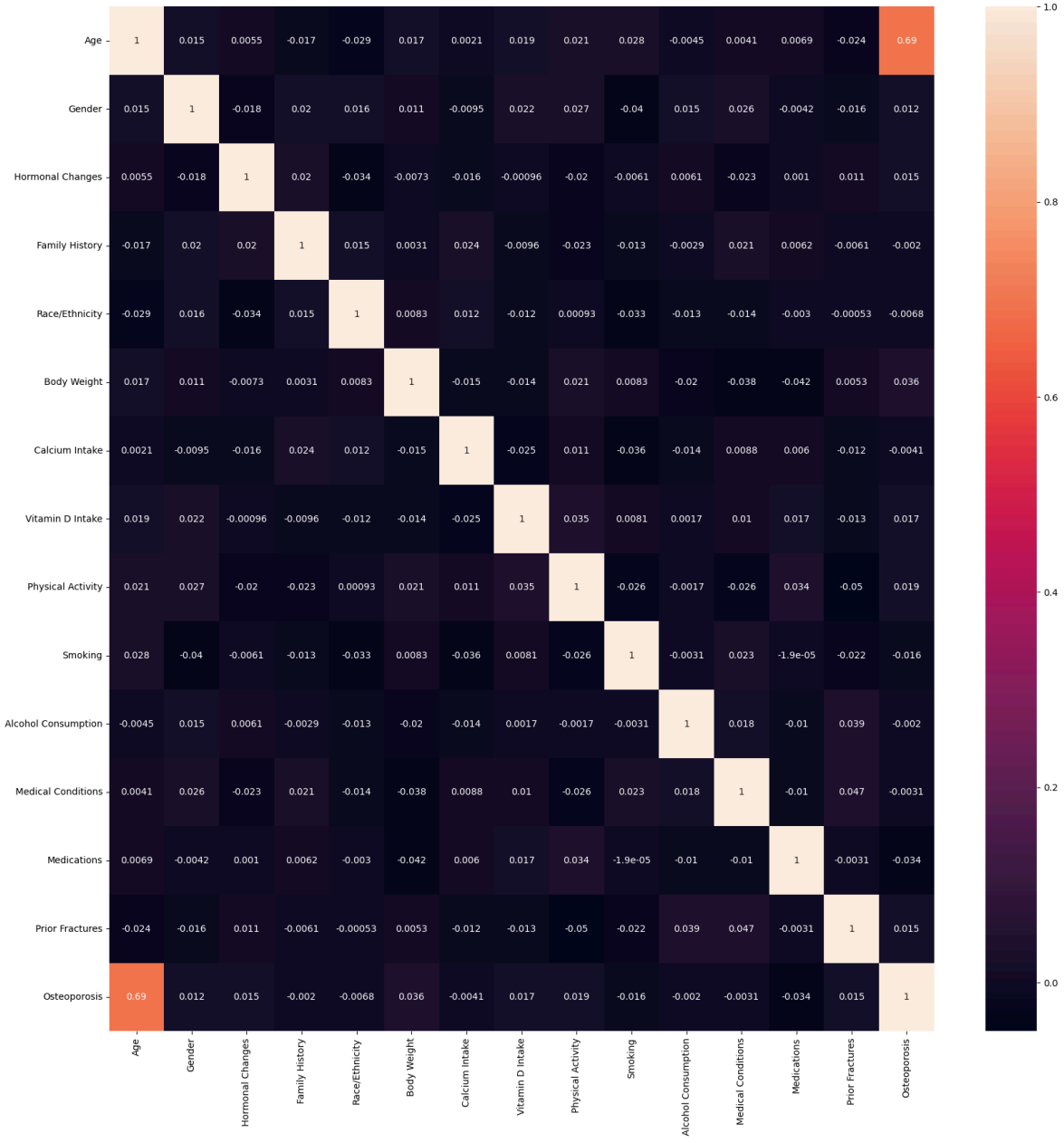
In [ ]:
```
#columns for label encoding
cols = df.select_dtypes(include=['object']).columns

#label encoding
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

for col in cols:
    df[col] = le.fit_transform(df[col])
    print(col,":",df[col].unique())
```

```
Gender : [0 1]
Hormonal Changes : [0 1]
Family History : [1 0]
Race/Ethnicity : [1 2 0]
Body Weight : [1 0]
Calcium Intake : [1 0]
Vitamin D Intake : [1 0]
Physical Activity : [1 0]
Smoking : [1 0]
Alcohol Consumption : [0 1]
Medical Conditions : [2 1 0]
Medications : [0 1]
Prior Fractures : [1 0]
```

Correlation Matrix Heatmap

In [ ]:
```
plt.figure(figsize=(20,20))
sns.heatmap(df.corr(), annot=True)
```

Out[ ]: <Axes: >



Train Test Split

In [ ]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(df.drop('Osteoporosis',axis=
```

Ostheoporosis Risk Prediction Models

For predicting the risk of osteoporosis, I will be using the following models:

- Logistic Regression
- Random Forest Classifier
- Decision Tree Classifier
- Support Vector Classifier

Logistic Regression

In [ ]:
```
from sklearn.linear_model import LogisticRegression

#creating logistic regression object
logmodel = LogisticRegression()
```

Hyperparameter Tuning using GridSearchCV

In [ ]:
```
from sklearn.model_selection import GridSearchCV

#parameters for grid search
param_grid = {'C': [0.1, 1, 10, 100, 1000],
              'penalty': ['l1', 'l2'],
              'solver': ['liblinear'],
              'max_iter': [100, 1000, 2500, 5000],
              'multi_class': ['auto', 'ovr'],
              'random_state': [0,42,101]}

#grid search object
grid = GridSearchCV(logmodel,param_grid,refit=True,verbose=3,cv=5,n_jobs=-1)

#fitting the data
grid.fit(X_train,y_train)

#best parameters
print(grid.best_params_)
```

```
Fitting 5 folds for each of 240 candidates, totalling 1200 fits
{'C': 0.1, 'max_iter': 100, 'multi_class': 'auto', 'penalty': 'l2', 'random_stat
e': 0, 'solver': 'liblinear'}
```

In [ ]:
```
#logistic regression with best parameters
logmodel = LogisticRegression(C=0.1, max_iter=100, penalty='l2', random_state=0,

#fitting the data
logmodel.fit(X_train,y_train)

#training accuracy
```

```
print("Training accuracy:",logmodel.score(X_train,y_train))

#prediction
lr_pred = logmodel.predict(X_test)
```

```
Training accuracy: 0.8284671532846716
```

Random Forest Classifier

In [ ]:
```
from sklearn.ensemble import RandomForestClassifier

#creating random forest object
rfc = RandomForestClassifier()
```

Hyperparameter Tuning using GridSearchCV

In [ ]:
```
#parameters for grid search
param_grid = {'criterion': ['gini', 'entropy'],
              'max_depth': [10, 20, 30],
              'min_samples_split': [2, 5, 10],
              'min_samples_leaf': [2,5,10],
              'random_state': [0,42,101]}

#grid search object
grid = GridSearchCV(rfc,param_grid,refit=True,verbose=3,cv=5,n_jobs=-1)

#fitting the data
grid.fit(X_train,y_train)

#best parameters
print(grid.best_params_)
```

```
Fitting 5 folds for each of 162 candidates, totalling 810 fits
{'criterion': 'gini', 'max_depth': 20, 'min_samples_leaf': 2, 'min_samples_spli
t': 2, 'random_state': 42}
```

In [ ]:
```
#random forest with best parameters
rfc = RandomForestClassifier(criterion='gini', max_depth=10, min_samples_leaf=2,

#fitting the data
rfc.fit(X_train,y_train)

#training accuracy
print("Training accuracy:",rfc.score(X_train,y_train))

#prediction
rfc_pred = rfc.predict(X_test)
```

```
Training accuracy: 0.9401459854014599
```

Decision Tree Classifier

In [ ]:
```
from sklearn.tree import DecisionTreeClassifier

#creating decision tree object
dtree = DecisionTreeClassifier()
```

Hyperparameter Tuning using GridSearchCV

In [ ]:
```
#parameters for grid search
param_grid = {'criterion': ['gini', 'entropy'],
              'max_depth': [10, 20, 30],
              'min_samples_split': [2, 5, 10],
              'min_samples_leaf': [2,5,10],
              'random_state': [0,42,101]}

#grid search object
grid = GridSearchCV(dtree,param_grid,refit=True,verbose=3,cv=5,n_jobs=-1)

#fitting the data
grid.fit(X_train,y_train)

#best parameters
print(grid.best_params_)
```

```
Fitting 5 folds for each of 162 candidates, totalling 810 fits
{'criterion': 'entropy', 'max_depth': 10, 'min_samples_leaf': 10, 'min_samples_sp
lit': 2, 'random_state': 0}
```

In [ ]:
```
#decision tree with best parameters
dtree = DecisionTreeClassifier(criterion='entropy', max_depth=10, min_samples_le

#fitting the data
dtree.fit(X_train,y_train)

#training accuracy
print("Training accuracy:",dtree.score(X_train,y_train))

#prediction
dtree_pred = dtree.predict(X_test)
```

```
Training accuracy: 0.9094890510948905
```

Support Vector Classifier

In [ ]:
```
from sklearn.svm import SVC

#creating support vector classifier object
svc = SVC()
```

Hyperparameter Tuning using GridSearchCV

In [ ]:
```
#parameters for grid search
param_grid = {'C': [0.1, 1, 10, 100],
              'degree': [2, 3, 4, 5],
              'gamma': ['scale', 'auto'],
              'random_state': [0,42,101]}

#grid search object
grid = GridSearchCV(svc,param_grid,refit=True,verbose=3,cv=5,n_jobs=-1)

#fitting the data
grid.fit(X_train,y_train)

#best parameters
print(grid.best_params_)
```

```
Fitting 5 folds for each of 96 candidates, totalling 480 fits
{'C': 1, 'degree': 2, 'gamma': 'auto', 'random_state': 0}
```

In [ ]:
```
#support vector classifier with best parameters
svc = SVC(C=0.1, degree=2, gamma='auto', random_state=0, kernel='linear')

#fitting the data
svc.fit(X_train,y_train)

#training accuracy
print("Training accuracy:",svc.score(X_train,y_train))

#prediction
svc_pred = svc.predict(X_test)
```

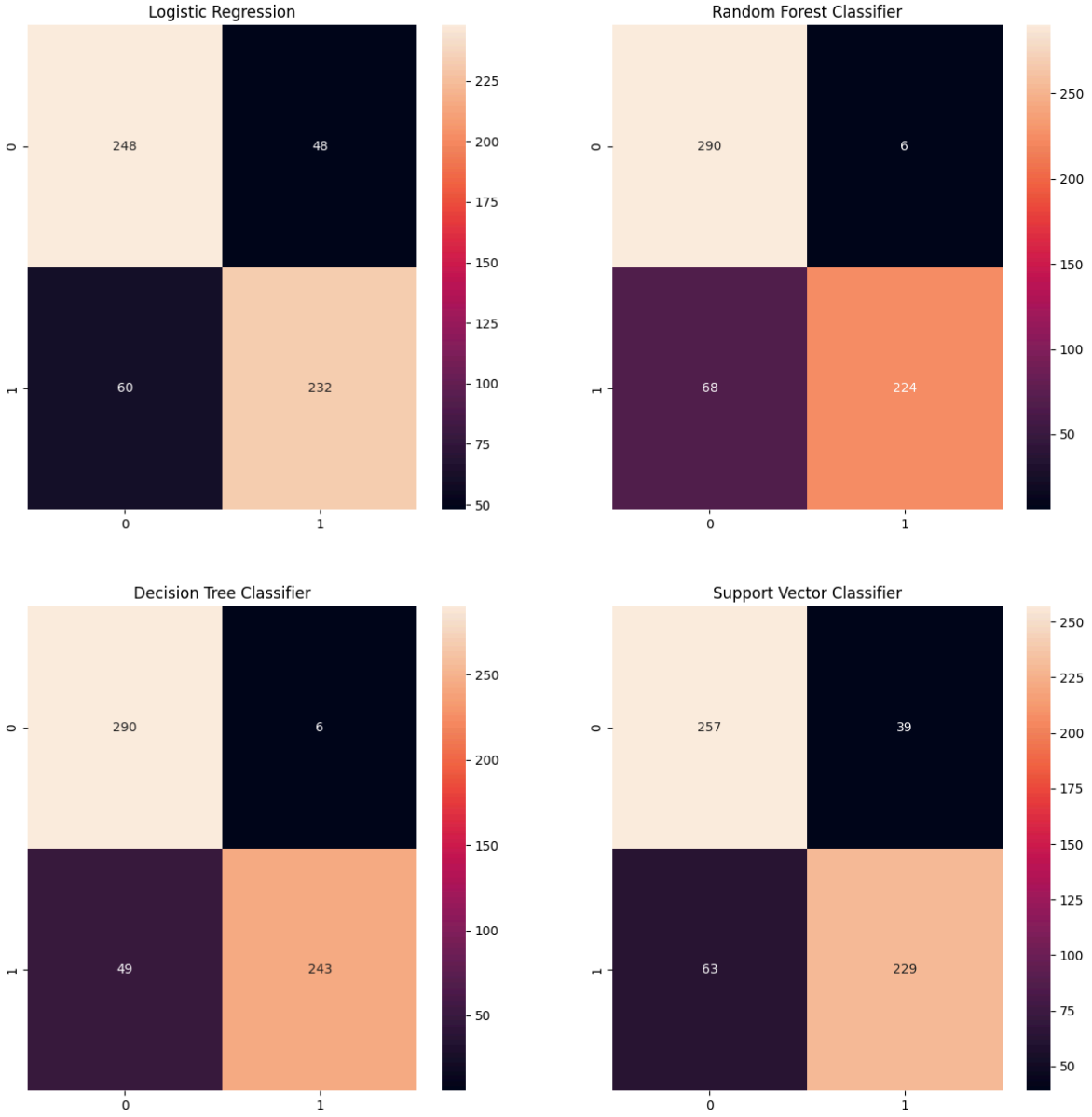
```
Training accuracy: 0.8350364963503649
```

Model Evaluation

Confusion Matrix

In [ ]:
```
from sklearn.metrics import confusion_matrix
fig, ax = plt.subplots(2, 2, figsize=(15, 15))

#confusion matrix for logistic regression
cm = confusion_matrix(y_test, lr_pred)
sns.heatmap(cm, annot=True, ax = ax[0,0], fmt='g').set_title('Logistic Regressio

#confusion matrix for random forest
cm = confusion_matrix(y_test, rfc_pred)
sns.heatmap(cm, annot=True, ax = ax[0,1], fmt='g').set_title('Random Forest Clas

#confusion matrix for decision tree
cm = confusion_matrix(y_test, dtree_pred)
sns.heatmap(cm, annot=True, ax = ax[1,0], fmt='g').set_title('Decision Tree Clas

#confusion matrix for support vector classifier
cm = confusion_matrix(y_test, svc_pred)
sns.heatmap(cm, annot=True, ax = ax[1,1], fmt='g').set_title('Support Vector Cla
```

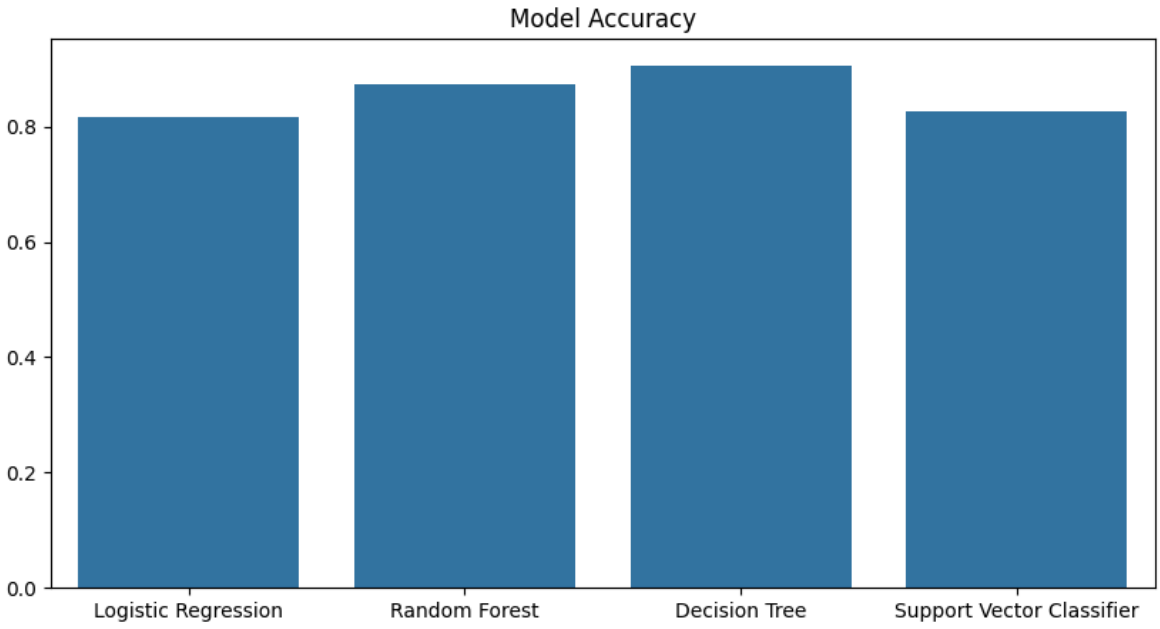
Out[ ]:
```
Text(0.5, 1.0, 'Support Vector Classifier')
```



Model Accuracy

In [ ]:
```
#Bar chart for the accuracy of the models
from sklearn.metrics import accuracy_score
models = ['Logistic Regression', 'Random Forest', 'Decision Tree', 'Support Vect
accuracy = [accuracy_score(y_test, lr_pred), accuracy_score(y_test, rfc_pred), a
plt.figure(figsize=(10,5))
sns.barplot(x=models, y=accuracy).set_title('Model Accuracy')
```

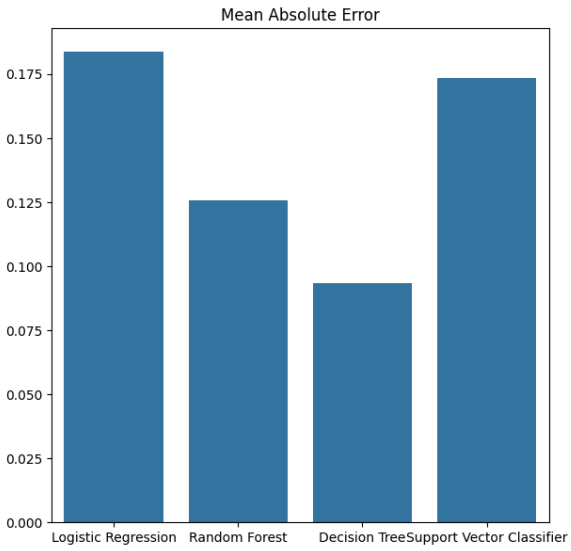
Out[ ]:
```
Text(0.5, 1.0, 'Model Accuracy')
```

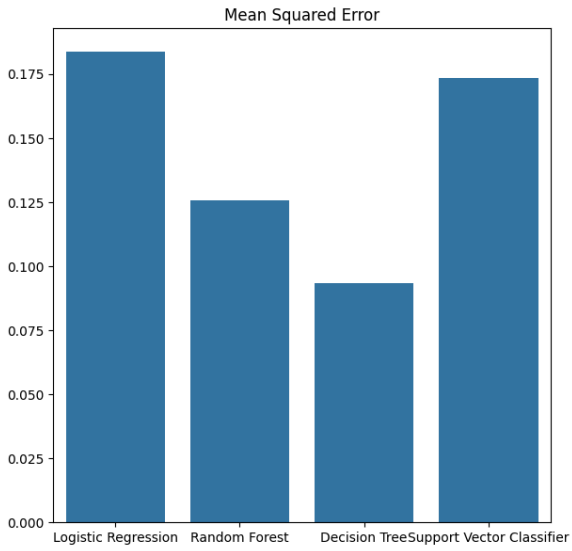


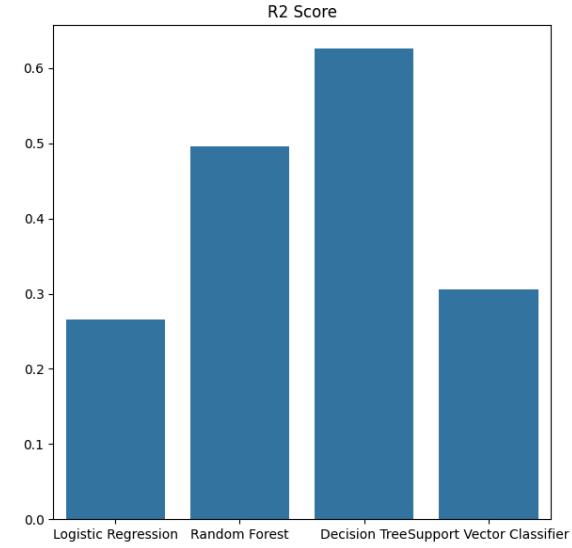
Model Metrics

In [ ]:
```
from sklearn.metrics import mean_absolute_error, mean_squared_error, r2_score, r

fig, ax = plt.subplots(2,2, figsize=(15, 15))
models = ['Logistic Regression', 'Random Forest', 'Decision Tree', 'Support Vect
mae = [mean_absolute_error(y_test, lr_pred), mean_absolute_error(y_test, rfc_pre
mse = [mean_squared_error(y_test, lr_pred), mean_squared_error(y_test, rfc_pred)
rmse = [np.sqrt(mean_squared_error(y_test, lr_pred)), np.sqrt(mean_squared_error
r2 = [r2_score(y_test, lr_pred), r2_score(y_test, rfc_pred), r2_score(y_test, dt

#Mean Absolute Error
sns.barplot(x=models, y=mae, ax=ax[0,0]).set_title('Mean Absolute Error')

#Mean Squared Error
sns.barplot(x=models, y=mse, ax=ax[0,1]).set_title('Mean Squared Error')

#Root Mean Squared Error
sns.barplot(x=models, y=rmse, ax=ax[1,0]).set_title('Root Mean Squared Error')

#R2 Score
sns.barplot(x=models, y=r2, ax=ax[1,1]).set_title('R2 Score')
```

Out[ ]:
```
Text(0.5, 1.0, 'R2 Score')
```







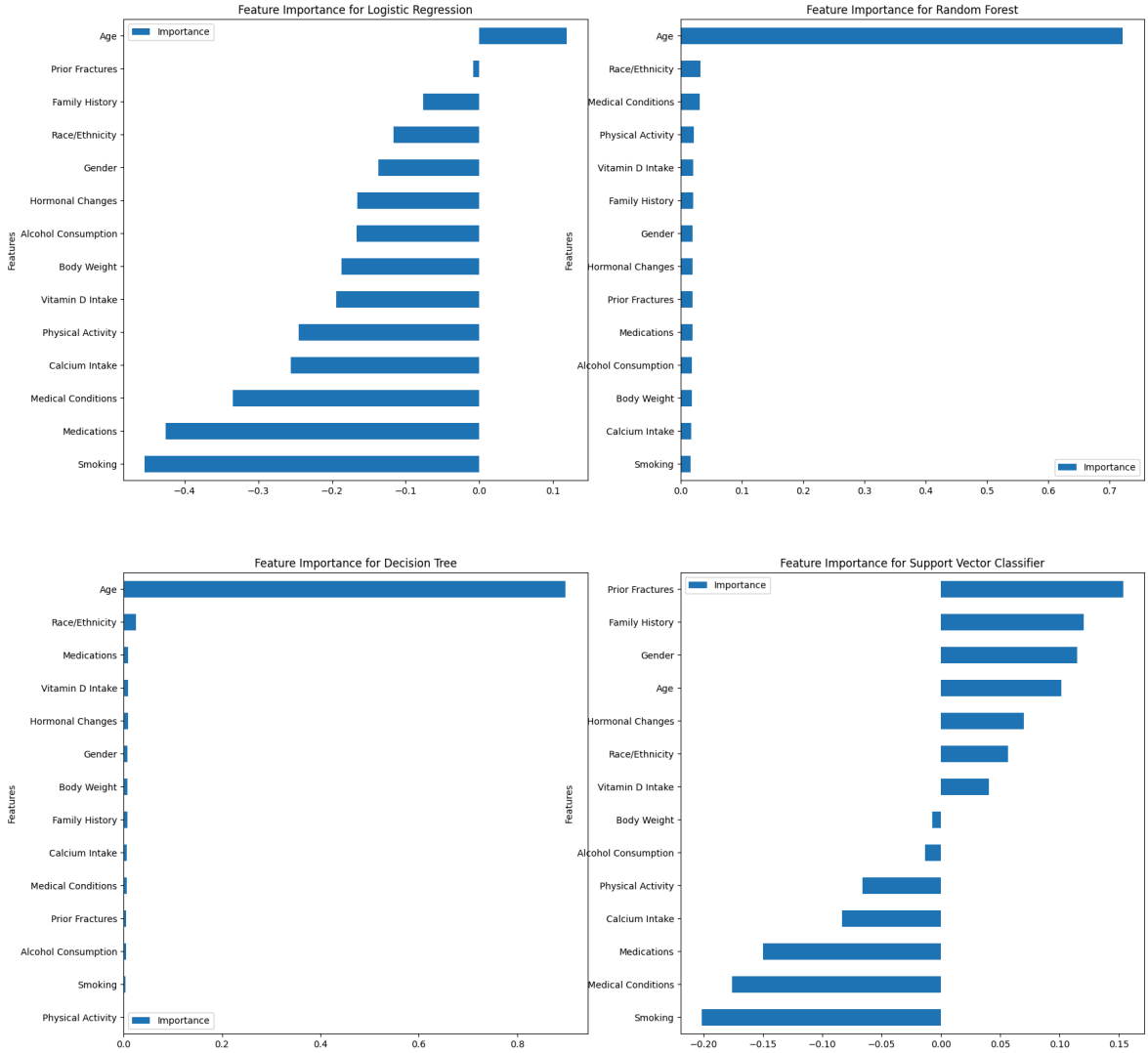
Feature Importance Analysis

In [ ]:

```
fig, ax = plt.subplots(2, 2, figsize=(20, 20))

#Feature Importance graph for Logistic Regression
coeff = list(logmodel.coef_[0])
labels = list(df.drop('Osteoporosis',axis=1).columns)
features = pd.DataFrame()
features['Features'] = labels
features['Importance'] = coeff
features.sort_values(by=['Importance'], ascending=True, inplace=True)
features = features.set_index('Features')
features.plot(kind='barh', ax=ax[0,0]).set_title('Feature Importance for Logisti

#Feature Importance graph for Random Forest
coeff = list(rfc.feature_importances_)
labels = list(df.drop('Osteoporosis',axis=1).columns)
features = pd.DataFrame()
features['Features'] = labels
features['Importance'] = coeff
features.sort_values(by=['Importance'], ascending=True, inplace=True)
features = features.set_index('Features')
features.plot(kind='barh', ax=ax[0,1]).set_title('Feature Importance for Random
```

```
#Feature Importance graph for Decision Tree
coeff = list(dtree.feature_importances_)
labels = list(df.drop('Osteoporosis',axis=1).columns)
features = pd.DataFrame()
features['Features'] = labels
features['Importance'] = coeff
features.sort_values(by=['Importance'], ascending=True, inplace=True)
features = features.set_index('Features')
features.plot(kind='barh', ax=ax[1,0]).set_title('Feature Importance for Decisio

#Feature Importance graph for Support Vector Classifier
coeff = list(svc.coef_[0])
labels = list(df.drop('Osteoporosis',axis=1).columns)
features = pd.DataFrame()
features['Features'] = labels
features['Importance'] = coeff
features.sort_values(by=['Importance'], ascending=True, inplace=True)
features = features.set_index('Features')
features.plot(kind='barh', ax=ax[1,1]).set_title('Feature Importance for Support
```

Out[ ]: Text(0.5, 1.0, 'Feature Importance for Support Vector Classifier')



Conclusion

In this project, I developed machine learning models to predict the risk of osteoporosis in patients based on their medical records. I analyzed the dataset, performed exploratory

data analysis, and developed predictive models using logistic regression, random forest classifier, decision tree classifier, and support vector classifier. I evaluated the models using confusion matrix, accuracy, precision, recall, and F1 score metrics.

From the exploratory data analysis, i have found that certain factors like Age, Hormona Changes, Medical Conditions, Medications, Lifestyle and nutrition are responsible for the risk of osteoporosis. Patients between 20-40 years of age have lower risk of osteoporosis. Patients who have undergone hormonal changes, have medical conditions, consume medications, have lower body weight, calcium and vitamin D levels, and have sedentary lifestyle have higher risk of osteoporosis.

Coming to the machine learning models, I have employed Logistic Regression, Random Tree, Decision Tree and Support Vector Classifier to predict the risk of osteoporosis based on the data. Out of these models, Decision Tree Classifier model gave the best results in comparison to others, with nearly 87% accuracy. The model can be used to predict the risk of osteoporosis in patients based on their medical records, enabling early intervention and prevention strategies.